After filter the poorly modeled Reads :

Original method :

① (Read likelihoods are exact)

	Allele : C		Allele : A	
	Hap ①	Hap ②	Hap ③	Hap ④
Read ①	1	2	3	4
Read ②	1	3	2	4
Read ③	2	3	1	4

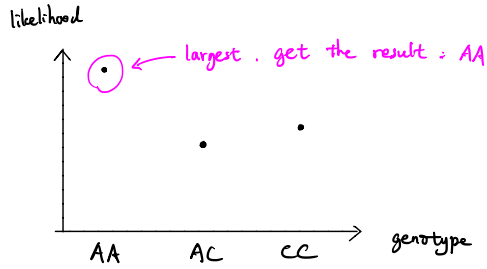
transform to Allele - Read Table ⟹

②

	Allele C	Allele A
Read ①	2	4
Read ②	3	4
Read ③	3	4

assign genotype likelihood.

③



Prune method :

① Read likelihoods only have bound values.

lowerbound :

	Allele : C		Allele : A	
	Hap ①	Hap ②	Hap ③	Hap ④
Read ①	1	2	3	1
Read ②	1	2	2	2
Read ③	1	3	1	1

upperbound :

	Hap ①	Hap ②	Hap ③	Hap ④
Read ①	1	3	3	2
Read ②	1	2	2	4
Read ③	2	3	1	2

⇓ When transform to Allele - Read Map ,
still pick the best of lower and upperbound

②

lower bound :

	Allele C	Allele A
Read ①	2	3
Read ②	2	2
Read ③	3	1

upperbound :

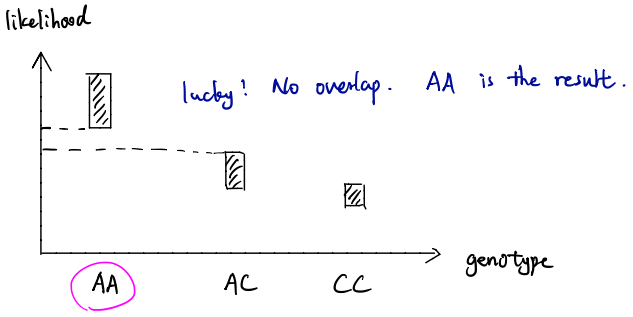
	Allele C	Allele A
Read ①	3	3
Read ②	2	4
Read ③	3	2

Note that best of lowerbound is still lowerbound
best of upperbound is still upperbound.

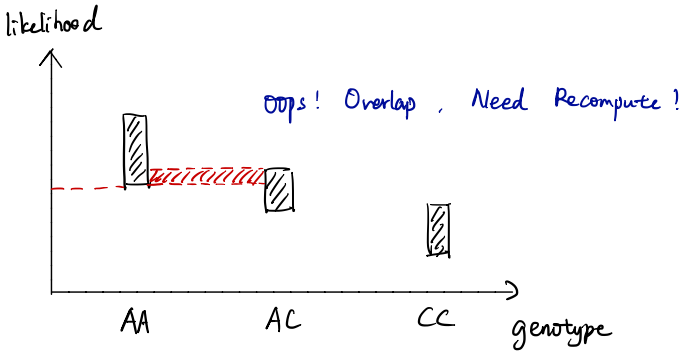
So the interval is still correct , but upperbound can be overestimated.

③ Now we assign genotype likelihoods according to last two matrices.

First case : No overlap



Second case : Overlap



⇓ Recompute Step

④ Return back to the matrix in ② :

lower bound:

	Allele C	Allele A
Read ①	2	3
Read ②	2	2
Read ③	3	1

⇐ The gap is 2! The largest one

upperbound :

	Allele C	Allele A
Read ①	3	3
Read ③	2	4
Read ③	3	2

How to decide which Read to recompute ? ⇒ Check the gap between lower and upperbound. The larger the gap is, the worse this read performs. (recompute !)

So we recompute read ② against Haplotype ③ and ④ (As they have allele "A")

⇓

Go back to step ③ . until it generates the exact result.